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Policies and politics of changing the food label

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Abstract

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Keywords

politics, policies, label, food, changing

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Food Safety and Health

Policies and Politics of Changing the Food Label

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Background: In 2010 a national comprehensive review of all food labelling law and policy was undertaken in Australia. The Australian governments accepted 21 of the 61 recommendations. This paper will outline the main recommendations from the review and will present the processes put into place to develop an interpretative front of pack labelling scheme. A cooperative approach involving government, public health and consumer groups and food industry representatives was undertaken.

Methods: Text and media analysis were undertaken. The Public Health Association of Australia was a participant observer in the committee processes that developed the Health Star Rating system. The timeline for committee work, key outcomes and recommendations and ministerial decisions were recorded. Subsequent media from both food industry groups (who backed away from the recommendations) and public health and government groups (who continued to support it) were tracked.

Results: The food industry was an active partner in the development of the health star rating system as the preferred front of pack labelling (FoPL) system recommended to Food Ministers. The system was approved to go forward for implementation within a two year period. Prior to and following the Ministers' decision there was a consistent attack by the food industry on this FoPL system aiming to have the decision reversed and undermining the co-regulatory policy approach.

Conclusions: The food industry never intended to agree with and support the implementation of a policy option that supported easier and healthier food choices by consumers. These findings support the WHO's recent stance that industry groups should not be at the policy-making table.

Keywords: food labelling, policy development, food industry

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Food Safety and Health

Rapid and High-Flux Identification of Clade or Sub-Clade 2.3.2 and 2.3.4 of Avian Influenza Virus Subtype H5N1

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Background: The highly pathogenic avian influenza (HPAI) virus, subtype H5N1, was first detected in 1996 in Southern China. Since then, the virus has spread to poultry and wild birds in more than 68 countries across Asia, the Middle East, Europe, and Africa and resulted in more than 384 human fatalities in 15 countries. Phylogenetic analysis of the HA gene of viruses indicated extensive genetic diversity. Multiple clades are present and clades 2.3.2 and 2.3.4 are predominant in many Asian and some European countries. Fast and high-flux identification of viral clade or sub-clade from clinical and field samples is very important for selecting correct candidate vaccine for effective control and prevention of influenza.

Methods: The rapid and high-flux method for identification of clade or sub-clade 2.3.2 and 2.3.4 had been designed based on multilocus nucleic acid sites and more than 96 samples can be analyzed at the same time by pyrosequencing.

Results: This allows the prediction of clade 2.3.2, 2.3.4 and sub-clade 2.3.2.1, 2.3.2.2, 2.3.4.2 and also viral strain, antigenic and receptor binding properties, low- or high-pathogenicity cleavage site and glycosylation status.

Conclusions: The method for rapid and high-flux identification of clade or sub-clade 2.3.2 and 2.3.4 of avian influenza virus subtype H5N1 had been established and implemented.

Keywords: Avian influenza virus, H5N1 subtype, Clade